

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: LONZA AG
- (B) STREET: Muenchensteinerstrasse 38
- (C) CITY: Basle
- (E) COUNTRY: Switzerland
- (F) POSTAL CODE: 4002

(ii) TITLE OF INVENTION: Process for the preparation of (S)- or (R)-3,3,3-trifluoro-2-hydroxy-2-methylpropionic acid

(iii) NUMBER OF SEQUENCES: 14

(iv) COMPUTER-READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (c) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: Nucleotide
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: Genomic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: Klebsiella oxytoca
- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(vii) PROVENANCE:

- (B) CLONE(S): pPRS2a

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(197..1181)
- (D) OTHER INFORMATION: /product= "amidase"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCCGGAACT CCATGTGGCC GTGATCCTGG TCGAGCAGGA TATTGCGATG ATCCAGCGGG	60
CCGCACAGCG CTGTGCGGTA ATGGATAAAG GCCTGGTTGT AGAAACGCTG ACCCAACAAC	120
AGCTCTCTGA TGATCTTTTA ATGCGTCGTC ATCTGGCTCT GTAACATAAC GCTATAAATT	180
ACGTGGAGAA TAACAT ATG AAA TGG TTG GAA GAA TCC ATT ATG GCC AAA	229
Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys	
1 5 10	

CGC GGT GTT GGT GCC GGG CGT AAA CCG GTA ACG CAT CAC CTG ACG GAA Arg Gly Val Gly Ala Gly Arg Lys Pro Val Thr His His Leu Thr Glu 15 20 25	277
GAA ATG CAA AAA GAG TTT CAT TAC ACC ATT GGC CCT TAT TCC ACA CCC Glu Met Gln Lys Glu Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro 30 35 40	325
GTC CTG ACC ATC GAA CCC GGT GAC CGG ATT ATT GTC GAC ACT CGA GAT Val Leu Thr Ile Glu Pro Gly Asp Arg Ile Ile Val Asp Thr Arg Asp 45 50 55	373
GCT TTT GAA GGT GCT ATC AAT TCG GAA CAG GAT ATT CCG AGC CAG TTG Ala Phe Glu Gly Ala Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln Leu 60 65 70 75	421
CTA AAA ATG CCC TTT CTC AAC CCA CAA AAC GGA CCG ATC ATG GTC AAT Leu Lys Met Pro Phe Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn 80 85 90	469
GGC GCG GAG AAA GGT GAT GTG CTC GCT GTC TAT ATC GAA TCC ATG TTG Gly Ala Glu Lys Gly Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu 95 100 105	517
CCC CGC GGC GTT GAT CCC TAC GGC ATC TGC GCC ATG ATT CCG CAT TTT Pro Arg Gly Val Asp Pro Tyr Gly Ile Cys Ala Met Ile Pro His Phe 110 115 120	565
GGC GGA CTG ACC GGG ACC GAC CTG ACG GCC ATG CTC AAT GAT CCG CTG Gly Gly Leu Thr Gly Thr Asp Leu Thr Ala Met Leu Asn Asp Pro Leu 125 130 135	613
CCA GAA AAG GTG CGC ATG ATT AAA CTC GAC AGT GAA AAG GTC TAC TGS Pro Glu Lys Val Arg Met Ile Lys Leu Asp Ser Glu Lys Val Tyr Trp 140 145 150 155	661
AGC AAA CGC CAT ACG CTT CCC TAT AAA CCC CAT ATT GGC ACC TTG AGC Ser Lys Arg His Thr Leu Pro Tyr Lys Pro His Ile Gly Thr Leu Ser 150 165 170	709
GTA TCG CCA GAA ATT GAC TCA ATC AAT TCA CTG ACG CCA GAC AAT CAC Val Ser Pro Glu Ile Asp Ser Ile Asn Ser Leu Thr Pro Asp Asn His 175 180 185	757
GGC GGG AAT ATG GAT GTG CCG GAT ATA GGA CCA GGG AGT ATT ACC TAT Gly Gly Asn Met Asp Val Pro Asp Ile Gly Pro Gly Ser Ile Thr Tyr 190 195 200	805
CTG CCG GTA CGT GCG CCT GGA GGC CGC CTG TTT ATT GGT GAT GCC CAT Leu Pro Val Arg Ala Pro Gly Gly Arg Leu Phe Ile Gly Asp Ala His 205 210 215	853
GCT TGT CAG GGT GAT GGT GAG ATT TGC GGG ACC GCA GTA GAG TTT GCC Ala Cys Gln Gly Asp Gly Glu Ile Cys Gly Thr Ala Val Glu Phe Ala 220 225 230 235	901
TCA ATC ACC ACC ATC AAA GTC GAT TTG ATC AAG AAC TGG CAG CTT TCC Ser Ile Thr Thr Ile Lys Val Asp Leu Ile Lys Asn Trp Gln Leu Ser 240 245 250	949
TGG CCA CGA ATG GAG AAT GCC GAA AAT ATT ATG AGT ATT GGC AGT GCA Trp Pro Arg Met Glu Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala 255 260 265	997

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CGT CCG CTG GAG GAT GCG ACG CGA ATT GCA TAT CGC GAC TTA ATT TAC      1045
Arg Pro Leu Glu Asp Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr
      270                      275                      280

TGG CTG GTA GAA GAC TTT GGC TTC GAA CAA TGG GAT GCC TAC ATG CTT      1093
Trp Leu Val Glu Asp Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu
      285                      290                      295

CTG AGT CAA TGC GGC AAA GTG CGG CTG GGC AAC ATG GTC GAC CCC AAA      1141
Leu Ser Gln Cys Gly Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys
      300                      305                      310                      315

TAC ACC GTT GGC GCG ATG CTG AAC AAA AAC CTG TTA GTT TAGTAGGAAT      1190
Tyr Thr Val Gly Ala Met Leu Asn Lys Asn Leu Leu Val
      320                      325

AACTAACCGG TGAACATTAC CCGGATGTAG ATCGGGGTAA TGTGTAAGTT CAAACAATCG      1250

CTATTTTAA CAGCTAAAGC AGGTGCATAT GGGGCCAGAT ACACCCATCA ATATTGGTTT      1310

ACTTTACTCC TTCAGCGGAG TGACGGCGGC ACAAGAGTTG TCACAATGGC GCGGAGCAAC      1370

CCAGGCTATT GCCGAAATTA ATCAAAATGG CGGCATCAAC GGCAGACCAC TCAATGCAAT      1430

TCATTGGAT CC                                                                1442

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala
 1                      5                      10                      15

Gly Arg Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys Glu
      20                      25                      30

Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile Glu
      35                      40                      45

Pro Gly Asp Arg Ile Ile Val Asp Thr Arg Asp Ala Phe Glu Gly Ala
      50                      55                      60

Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln Leu Leu Lys Met Pro Phe
      65                      70                      75                      80

Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala Glu Lys Gly
      85                      90                      95

Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg Gly Val Asp
      100                      105                      110

Pro Tyr Gly Ile Cys Ala Met Ile Pro His Phe Gly Gly Leu Thr Gly
      115                      120                      125

Thr Asp Leu Thr Ala Met Leu Asn Asp Pro Leu Pro Glu Lys Val Arg
      130                      135                      140

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Met Ile Lys Leu Asp Ser Glu Lys Val Tyr Trp Ser Lys Arg His Thr
 145 150 155 160
 Leu Pro Tyr Lys Pro His Ile Gly Thr Leu Ser Val Ser Pro Glu Ile
 165 170 175
 Asp Ser Ile Asn Ser Leu Thr Pro Asp Asn His Gly Gly Asn Met Asp
 180 185 190
 Val Pro Asp Ile Gly Pro Gly Ser Ile Thr Tyr Leu Pro Val Arg Ala
 195 200 205
 Pro Gly Gly Arg Leu Phe Ile Gly Asp Ala His Ala Cys Gln Gly Asp
 210 215 220
 Gly Glu Ile Cys Gly Thr Ala Val Glu Phe Ala Ser Ile Thr Thr Ile
 225 230 235 240
 Lys Val Asp Leu Ile Lys Asn Trp Gln Leu Ser Trp Pro Arg Met Glu
 245 250 255
 Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg Pro Leu Glu Asp
 260 265 270
 Ala Thr Arg Ile Ala Tyr Arg Asp Leu Ile Tyr Trp Leu Val Glu Asp
 275 280 285
 Phe Gly Phe Glu Gln Trp Asp Ala Tyr Met Leu Leu Ser Gln Cys Gly
 290 295 300
 Lys Val Arg Leu Gly Asn Met Val Asp Pro Lys Tyr Thr Val Gly Ala
 305 310 315 320
 Met Leu Asn Lys Asn Leu Leu Val
 325

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Lys Trp Leu Glu Glu Ser Ile Met Ala Lys Arg Gly Val Gly Ala
 1 5 10 15
 Ser Arg Lys Pro
 20

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Val Tyr Trp Ser Lys

1

5

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Lys Pro Val Thr His His Leu Thr Glu Glu Met Gln Lys

1

5

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Tyr Thr Val Gly Ala Met Leu Asn Lys

1

5

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Glu Asn Ala Glu Asn Ile Met Ser Ile Gly Ser Ala Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Trp Leu Glu Glu Ser Ile Met Ala Lys
1 5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: not known

(D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

(B) STRAIN: PRS1

(C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Met Pro Phe Leu Asn Pro Gln Asn Gly Pro Ile Met Val Asn Gly Ala
1 5 10 15

Glu Lys

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Ala Phe Glu Gly Ala Ile Asn Ser Glu Gln Asp Ile Pro Ser Gln
1 5 10 15

Leu Leu Lys

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Phe His Tyr Thr Ile Gly Pro Tyr Ser Thr Pro Val Leu Thr Ile
1 5 10 15

Glu Pro Gly Asp Arg
20

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Phe Ile Gly Asp Ala His Ala Glu Gln Gly Asp Gly Glu Ile Glu

1 5 10 15

Gly Thr Ala Val Glu Phe Ala
20

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (B) STRAIN: PRS1
- (C) INDIVIDUAL/ISOLATE: PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Gly Asp Val Leu Ala Val Tyr Ile Glu Ser Met Leu Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not known
- (D) TOPOLOGY: not known

(ii) MOLECULE TYPE: peptide

(vi) ORIGIN:

- (C) INDIVIDUAL/ISOLATE: PRS1

(vii) PROVENANCE:

- (B) CLONE(S): PRS1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Gly Val Asp Pro Tyr Gly Ile Glu Ala Met Ile Pro His Phe Gly Gly
1 5 10 13

Leu Thr Gly Thr Asp Leu Thr Ala Met Leu Asn Asp Gln Leu Gln Pro
20 25 30

Lys